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## RAW SEQUENCE LISTING

DATE: 12/06/2001

PATENT APPLICATION: US/09/965,553

TIME: 11:36:05

Input Set : N:\Crf3\RULE60\09965553.txt

Output Set: N:\CRF3\12062001\I965553.raw

5 <110> APPLICANT: Wright, David A.  
7 Voytas, Daniel F.  
11 <120> TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto  
15 <130> FILE REFERENCE: P-1065 ISURF Plant Retroelement  
19 <140> CURRENT APPLICATION NUMBER: 09/965,553  
20 <141> CURRENT FILING DATE: 2001-09-27  
22 <150> PRIOR APPLICATION NUMBER: 09/322,478  
23 <151> PRIOR FILING DATE: 1999-05-28  
27 <150> PRIOR APPLICATION NUMBER: 60/087125  
29 <151> PRIOR FILING DATE: 1998-05-29  
33 <160> NUMBER OF SEQ ID NOS: 41  
37 <170> SOFTWARE: PatentIn Ver. 2.0  
41 <210> SEQ ID NO: 1  
43 <211> LENGTH: 18  
45 <212> TYPE: DNA  
47 <213> ORGANISM: Glycine max  
51 <400> SEQUENCE: 1  
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59 <211> LENGTH: 18  
61 <212> TYPE: DNA  
63 <213> ORGANISM: Glycine max  
67 <400> SEQUENCE: 2  
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73 <210> SEQ ID NO: 3  
75 <211> LENGTH: 6  
77 <212> TYPE: DNA  
79 <213> ORGANISM: Glycine max  
83 <400> SEQUENCE: 3  
85 ttgggg 6  
89 <210> SEQ ID NO: 4  
91 <211> LENGTH: 7  
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95 <213> ORGANISM: Artificial Sequence  
99 <220> FEATURE:  
101 <223> OTHER INFORMATION: Description of Artificial Sequence: plant  
103 retroelement sequence  
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111 1 5  
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119 <211> LENGTH: 1263  
121 <212> TYPE: DNA  
123 <213> ORGANISM: Artificial Sequence  
127 <220> FEATURE:  
129 <223> OTHER INFORMATION: Description of Artificial Sequence: plant  
131 retroelement sequence

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135 &lt;400&gt; SEQUENCE: 5

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137 atggcctccc gtaaacgcaa agctgtgccc acacccgggg aagcgtccaa ctgggactct 60
139 tcacgtttca ctttcgagat tgcttggcac agataccagg atagcattca gctccggaac 120
141 atccttccag agaggaatgt agagcttggg ccagggatgt ttgatgagtt cctgcaggaa 180
143 ctccagaggg tcagatggga ccaggttctg acccgacttc cagagaagtg gattgatgtt 240
145 gctctgggtg aggagtttta ctccaacctt tatgatccag aggaccacag tccgaagtgt 300
147 tggagtgttc gaggacaggt tgtgagattt gatgctgaga cgattaatga tttcctcgac 360
149 accccgggtc tcttggcaga gggagaggat tatccagcct actctcagta cctcagcact 420
151 cctccagacc atgatgccat cctttccgct ctgtgtactc cagggggacg atttgttctg 480
153 aatgttgata gtgccccctg gaagctgctg cggaaggatc tgatgacgct cgcgcagaca 540
155 tggagtgtgc tctcttattt taaccttgca ctgacttttc acactttctg tattaatgtt 600
157 gacagggccc gactcaatta tggcttggtg atgaagatgg acctggacgt gggcagcctc 660
159 atttctcttc agatcagtcg gatcgcccag tccatcactt ccaggcttgg gttcccagcg 720
161 ttgatcacia cactgtgtga gattcagggg gttgtctctg ataccctgat ttttgagtca 780
163 ctcatgcttg tgatcaacct tgcctacatt aagaagaact gctggaaccc tgccgatcca 840
165 tctatcacat ttcaggggac ccgccgcacg cgcaccagag ctccggcgct gccatctgag 900
167 gctcctcttc catcccagca tccttctcag cctttttccc agagaccacg gcctccactt 960
169 ctatccacct cagcacctcc atacatgcat ggacagatgc tcaggctcct gtaccagggg 1020
171 cagcagatca tcattcagaa cctgtatcga ttgtccctac atttgacgat ggatctgcca 1080
173 ctcatgactc cggaggccta tcgtcagcag gtcgccaagc taggagacca gccctccact 1140
175 gacagggggg aagagccttc tggagccgct gctactgagg atcctgccgt tgatgaagac 1200
177 ctcatagctg acttggtctg cgctgattgg agcccatggg cagacttggg cagaggcagc 1260
179 tga 1263

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183 &lt;210&gt; SEQ ID NO: 6

185 &lt;211&gt; LENGTH: 421

187 &lt;212&gt; TYPE: PRT

189 &lt;213&gt; ORGANISM: Artificial Sequence

193 &lt;220&gt; FEATURE:

195 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: plant

197 retroelement sequence

201 &lt;400&gt; SEQUENCE: 6

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203 Met Ala Ser Arg Lys Arg Lys Ala Val Pro Thr Pro Gly Glu Ala Ser
205 1 5 10 15
209 Asn Trp Asp Ser Ser Arg Phe Thr Phe Glu Ile Ala Trp His Arg Tyr
211 20 25 30
215 Gln Asp Ser Ile Gln Leu Arg Asn Ile Leu Pro Glu Arg Asn Val Glu
217 35 40 45
221 Leu Gly Pro Gly Met Phe Asp Glu Phe Leu Gln Glu Leu Gln Arg Leu
223 50 55 60
227 Arg Trp Asp Gln Val Leu Thr Arg Leu Pro Glu Lys Trp Ile Asp Val
229 65 70 75 80
233 Ala Leu Val Lys Glu Phe Tyr Ser Asn Leu Tyr Asp Pro Glu Asp His
235 85 90 95
239 Ser Pro Lys Phe Trp Ser Val Arg Gly Gln Val Val Arg Phe Asp Ala
241 100 105 110
245 Glu Thr Ile Asn Asp Phe Leu Asp Thr Pro Val Ile Leu Ala Glu Gly
247 115 120 125
251 Glu Asp Tyr Pro Ala Tyr Ser Gln Tyr Leu Ser Thr Pro Pro Asp His
253 130 135 140

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257 Asp Ala Ile Leu Ser Ala Leu Cys Thr Pro Gly Gly Arg Phe Val Leu
259 145          150          155          160
263 Asn Val Asp Ser Ala Pro Trp Lys Leu Leu Arg Lys Asp Leu Met Thr
265          165          170          175
269 Leu Ala Gln Thr Trp Ser Val Leu Ser Tyr Phe Asn Leu Ala Leu Thr
271          180          185          190
275 Phe His Thr Ser Asp Ile Asn Val Asp Arg Ala Arg Leu Asn Tyr Gly
277          195          200          205
281 Leu Val Met Lys Met Asp Leu Asp Val Gly Ser Leu Ile Ser Leu Gln
283          210          215          220
287 Ile Ser Gln Ile Ala Gln Ser Ile Thr Ser Arg Leu Gly Phe Pro Ala
289 225          230          235          240
293 Leu Ile Thr Thr Leu Cys Glu Ile Gln Gly Val Val Ser Asp Thr Leu
295          245          250          255
299 Ile Phe Glu Ser Leu Ser Pro Val Ile Asn Leu Ala Tyr Ile Lys Lys
301          260          265          270
305 Asn Cys Trp Asn Pro Ala Asp Pro Ser Ile Thr Phe Gln Gly Thr Arg
307          275          280          285
311 Arg Thr Arg Thr Arg Ala Ser Ala Ser Ala Ser Glu Ala Pro Leu Pro
313          290          295          300
317 Ser Gln His Pro Ser Gln Pro Phe Ser Gln Arg Pro Arg Pro Pro Leu
319 305          310          315          320
323 Leu Ser Thr Ser Ala Pro Pro Tyr Met His Gly Gln Met Leu Arg Ser
325          325          330          335
329 Leu Tyr Gln Gly Gln Gln Ile Ile Ile Gln Asn Leu Tyr Arg Leu Ser
331          340          345          350
335 Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg
337          355          360          365
341 Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu
343          370          375          380
347 Glu Pro Ser Gly Ala Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp
349 385          390          395          400
353 Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu
355          405          410          415
359 Gly Arg Gly Ser Glx
361          420
367 <210> SEQ ID NO: 7
369 <211> LENGTH: 1596
371 <212> TYPE: DNA
373 <213> ORGANISM: Artificial Sequence
377 <220> FEATURE:
379 <223> OTHER INFORMATION: Description of Artificial Sequence: plant
381      retroelement sequence
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389 tgtcggcgta acaacgctgc aagaagaaga agggagcaag acatagaagg aagtagttac 120
391 acctcacctc ctcttctctc aaattatgct cagatggacg gggaaccggc acaaagagtc 180
393 acactagagg acttctctaa taccaccact cctcagttct ttacaagtat cacaaggccg 240
395 gaagtccaag cagatctcct tactcaaggg aacctcttcc atggtcttcc aaatgaagat 300

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397 ccatatgcgc atctagcctc atacatagag atatgcagca ccgttaaaat cgccggagtt 360
399 ccaaaagatg cgatactcct taacctcttt tccttttccc tagcaggaga ggcaaaaaga 420
401 tggttgcact ccttttaaagg caatagctta agaacatggg aagaagtagt ggaaaaattc 480
403 ttaaagaagt atttcccaga gtcaaagacc gtcgaacgaa agatggagat ttcttatttc 540
405 catcaatttc tggatgaatc ccttagcgaa gcactagacc atttccacgg attgctaaga 600
407 aaaacaccaa cacacagata cagcgagcca gtacaactaa acatattcat cgatgacttg 660
409 caactcttaa tcgaaacagc tactagaggg aagatcaagc tgaagactcc cgaagaagcg 720
411 atggagctcg tcgagaacat ggcggctagc gatcaagcaa tccttcatga tcacacttat 780
413 gttcccacaa aaagaagcct cttggagctt agcacgcagg acgcaacttt ggtacaaaac 840
415 aagctgttga cgaggcagat agaagccctc atcgaaaccc tcagcaagct gcctcaacaa 900
417 ttacaagcga taagttcttc ccactcttct gttttgcagg tagaagaatg ccccatatgc 960
419 agagggacac atgagcctgg acaatgtgca agccaacaag acccctctcg tgaagtaa 1020
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423 ttcaatcaag gggcaacaag atttaatcac gagccaccgg ggtttaatca aggaagaaac 1140
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427 ccaccatacc agccaccata ccagcaccct agccaagggtc cgaatcagca agaaaagccc 1260
429 accaaaatag aggaactgct gctgcaattc atcaaggaga caagatcaca tcaaaagagc 1320
431 acggatgcag ccattcggaa tctagaagtt caaatgggcc aactggcgca tgacaaagcc 1380
433 gaacggccca ctagaacttt cgggtgctaac atggagagaa gaaccccaag gaaggataaa 1440
435 gcagtactga ctagagggca gagaagagcg caggaggagg gtaagggtga aggagaagac 1500
437 tggccagaag aagggaaggac agagaagaca gaagaagaag agaaggtggc agaagaacct 1560
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443 &lt;210&gt; SEQ ID NO: 8

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447 &lt;212&gt; TYPE: PRT

449 &lt;213&gt; ORGANISM: Artificial Sequence

453 &lt;220&gt; FEATURE:

455 <223> OTHER INFORMATION: Description of Artificial Sequence: plant  
 457 retroelement sequence

461 &lt;400&gt; SEQUENCE: 8

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465 1 5 10 15

469 Ile Glu Ala Thr Cys Arg Arg Asn Asn Ala Ala Arg Arg Arg Arg Glu

471 20 25 30

475 Gln Asp Ile Glu Gly Ser Ser Tyr Thr Ser Pro Pro Pro Ser Pro Asn

477 35 40 45

481 Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp

483 50 55 60

487 Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro

489 65 70 75 80

493 Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu

495 85 90 95

499 Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys

501 100 105 110

505 Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn

507 115 120 125

511 Leu Phe Ser Phe Ser Leu Ala Gly Glu Ala Lys Arg Trp Leu His Ser

513 130 135 140

517 Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe

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519 145          150          155          160
523 Leu Lys Lys Tyr Phe Pro Glu Ser Lys Thr Val Glu Arg Lys Met Glu
525          165          170          175
529 Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu
531          180          185          190
535 Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser
537          195          200          205
541 Glu Pro Val Gln Leu Asn Ile Phe Ile Asp Asp Leu Gln Leu Leu Ile
543          210          215          220
547 Glu Thr Ala Thr Arg Gly Lys Ile Lys Leu Lys Thr Pro Glu Glu Ala
549 225          230          235          240
553 Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His
555          245          250          255
559 Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr
561          260          265          270
565 Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu
567          275          280          285
571 Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile
573          290          295          300
577 Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys
579 305          310          315          320
583 Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser
585          325          330          335
589 Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly
591          340          345          350
595 Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe
597          355          360          365
601 Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly
603          370          375          380
607 Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln
609 385          390          395          400
613 Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln
615          405          410          415
619 Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Leu Gln Phe Ile Lys
621          420          425          430
625 Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu
627          435          440          445
631 Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr
633          450          455          460
637 Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys
639 465          470          475          480
643 Ala Val Leu Thr Arg Gly Gln Arg Arg Ala Gln Glu Glu Gly Lys Val
645          485          490          495
649 Glu Gly Glu Asp Trp Pro Glu Glu Gly Arg Thr Glu Lys Thr Glu Glu
651          500          505          510
655 Glu Glu Lys Val Ala Glu Glu Pro Lys Arg Thr Lys Ser Gln Arg Ala
657          515          520          525
661 Arg Glu Ala Lys
663          530

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## VERIFICATION SUMMARY

DATE: 12/06/2001

PATENT APPLICATION: US/09/965,553

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